



#0

SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT
OF CARIES

<130> P04885US1

<140> 09/833,017

<141> 2001-04-10

<150> PCT/CA00/00605

<151> 2000-05-25

<150> 2,302,861

<151> 2000-04-10

<150> 2,332,733

<151> 2001-02-20

<160> 28

<170> PatentIn version 3.0

<210> 1

<211> 141

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(141)

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gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

<210> 2

<211> 46

<212> PRT

<213> Streptococcus mutans

<400> 2

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
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20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<222> (1)..(1326)

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acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240

Pro	Leu	Tyr	Phe	Ile	Ala	Leu	Ser	Ile	Tyr	Leu	Asn	Arg	Gln	Asn	Ser		
65					70					75					80		
ctt	tct	cta	aat	ata	ttt	tat	ggg	ctg	ctg	cct	gtt	gcc	agt	tct	gac	288	
Leu	Ser	Leu	Asn	Ile	Phe	Tyr	Gly	Leu	Leu	Pro	Val	Ala	Ser	Ser	Asp		
			85					90					95				
ttg	ttt	agg	cgg	gca	atc	ata	ttc	ttt	atc	ttg	gat	gga	act	caa	gga	336	
Leu	Phe	Arg	Arg	Ala	Ile	Ile	Phe	Phe	Ile	Leu	Asp	Gly	Thr	Gln	Gly		
			100					105					110				
att	gta	atg	ggc	agt	agc	att	ata	acc	acc	tat	atg	atc	gag	ttt	gca	384	
Ile	Val	Met	Gly	Ser	Ser	Ile	Ile	Thr	Thr	Tyr	Met	Ile	Glu	Phe	Ala		
		115						120					125				
gga	ata	gcg	cta	agt	tac	ctc	ttt	ctc	agt	gtg	ttc	aat	gtt	gat	att	432	
Gly	Ile	Ala	Leu	Ser	Tyr	Leu	Phe	Leu	Ser	Val	Phe	Asn	Val	Asp	Ile		
	130						135					140					
ggg	cga	ctt	aaa	gat	agt	ttg	acc	aag	atg	aag	gtc	aaa	aaa	cgc	ttg	480	
Gly	Arg	Leu	Lys	Asp	Ser	Leu	Thr	Lys	Met	Lys	Val	Lys	Lys	Arg	Leu		
145					150					155					160		
att	cca	atg	aat	att	act	atg	ctt	cta	tac	tac	ctt	tta	ata	cag	gta	528	
Ile	Pro	Met	Asn	Ile	Thr	Met	Leu	Leu	Tyr	Tyr	Leu	Leu	Ile	Gln	Val		
			165						170					175			
ttg	tat	gtt	ata	gag	agt	tat	aat	gtg	ata	ccg	act	tta	aaa	ttt	cgt	576	
Leu	Tyr	Val	Ile	Glu	Ser	Tyr	Asn	Val	Ile	Pro	Thr	Leu	Lys	Phe	Arg		
		180						185					190				
aaa	ttt	gtc	gtt	att	gtc	tat	ctt	att	tta	ttt	ttg	att	ctg	atc	tca	624	
Lys	Phe	Val	Val	Ile	Val	Tyr	Leu	Ile	Leu	Phe	Leu	Ile	Leu	Ile	Ser		
		195					200					205					
ttt	tta	agc	caa	tat	acc	aaa	caa	aag	gtt	caa	aat	gag	ata	atg	gca	672	
Phe	Leu	Ser	Gln	Tyr	Thr	Lys	Gln	Lys	Val	Gln	Asn	Glu	Ile	Met	Ala		
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caa	aag	gaa	gct	cag	att	cga	aat	atc	acc	cag	tat	agt	cag	caa	ata	720	
Gln	Lys	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Thr	Gln	Tyr	Ser	Gln	Gln	Ile		
225					230					235					240		
gaa	tct	ctt	tac	aag	gat	att	cga	agt	ttc	cgc	cat	gat	tat	ctg	aat	768	
Glu	Ser	Leu	Tyr	Lys	Asp	Ile	Arg	Ser	Phe	Arg	His	Asp	Tyr	Leu	Asn		
			245						250					255			
att	tta	act	agc	ctc	aga	tta	ggc	att	gaa	aat	aaa	gat	tta	gct	agt	816	
Ile	Leu	Thr	Ser	Leu	Arg	Leu	Gly	Ile	Glu	Asn	Lys	Asp	Leu	Ala	Ser		
		260						265					270				
att	gaa	aag	att	tac	cat	caa	atc	tta	gaa	aaa	aca	gga	cat	caa	ttg	864	
Ile	Glu	Lys	Ile	Tyr	His	Gln	Ile	Leu	Glu	Lys	Thr	Gly	His	Gln	Leu		
		275					280					285					
cag	gat	acc	cgt	tat	aat	atc	ggc	cat	cta	gct	aat	att	caa	aac	gat	912	
Gln	Asp	Thr	Arg	Tyr	Asn	Ile	Gly	His	Leu	Ala	Asn	Ile	Gln	Asn	Asp		

290	295	300	
gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa			960
Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys			
305	310	315	320
aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag			1008
Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu			
	325	330	335
atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat			1056
Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn			
	340	345	350
gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc			1104
Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala			
	355	360	365
ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc			1152
Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr			
	370	375	380
aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc			1200
Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser			
385	390	395	400
act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att			1248
Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile			
	405	410	415
ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat			1296
Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His			
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tta ttc aag caa ctc cta ata ata aaa tag			1326
Leu Phe Lys Gln Leu Leu Ile Ile Lys			
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<210> 4

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<212> PRT

<213> Streptococcus mutans

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Thr	Val	Leu	Phe	Leu	Leu	Phe	Leu	Phe	Ser	Lys	Val	Ser	Asn	Val	Thr
			20					25					30		

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
 35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
 50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
 65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
 85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
 100 105 110

Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
 115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
 130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
 145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
 165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
 180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
 195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
 210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
 225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
 245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
405 410 415

Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
420 425 430

Leu Phe Lys Gln Leu Leu Ile Ile Lys
435 440

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<211> 750

<212> DNA

<213> Streptococcus mutans

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<221> CDS

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ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat 96
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
20 25 30

aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc 144
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
35 40 45

cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa 192
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
50 55 60

aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat 240
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
65 70 75 80

aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg 288
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
85 90 95

ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa 336
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
100 105 110

tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat 384
Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
115 120 125

tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt 432
Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
130 135 140

att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att 480
Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
145 150 155 160

ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act 528
Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa 576
Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys

180	185	190	
atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct			624
Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro			
195	200	205	
gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga			672
Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg			
210	215	220	
aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga			720
Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg			
225	230	235	240
gct gtg att gct gat caa agg aga gca aaa			750
Ala Val Ile Ala Asp Gln Arg Arg Ala Lys			
245	250		
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<213> Streptococcus mutans			
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Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr			
20	25	30	
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile			
35	40	45	
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys			
50	55	60	
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His			
65	70	75	80
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met			
85	90	95	
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys			
100	105	110	

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
 115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
 130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
 145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
 165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
 180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
 195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
 210 215 220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
 225 230 235 240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
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<210> 7

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<212> PRT

<213> Streptococcus mutans

<220>

<221> PEPTIDE

<222> (1)..(46)

<400> 7

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
 20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
 35 40 45

<210> 8

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<213> Streptococcus mutans

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<222> (1)..(46)

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 1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
 20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
 35 40 45

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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<222> (1)..(43)

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala
35 40

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<212> PRT

<213> Streptococcus mutans

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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<213> synthetic construct

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<221> PEPTIDE

<222> (1)..(21)

<400> 14

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Gln Ala Leu Gly Lys
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<210> 15

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<212> DNA

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<222> (1)..(19)

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<222> (1)..(24)

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<210> 18

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<213> synthetic construct

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<222> (1)..(21)

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gcttcctttt gtgccattat c

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<210> 19

<211> 21

<212> DNA

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<222> (1)..(21)

<400> 19

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21

<210> 20

<211> 22

<212> DNA

<213> synthetic construct

<220>

<221> STS

<222> (1)..(22)

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 <212> DNA
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 <221> misc_feature
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 aaaaaatgac tttaaagaaa ttaagactga tgaattagag attatcattg gcggaagcgg 180
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tatctttaag	tcgaccaata	tcaacattga	acacactgag	aaagaggtaa	cttagcgcta	1320
ttcctgcaaa	ctcgatcata	taggtgggta	taatgctact	gccattaca	attccttgag	1380
ttccatccaa	gataaagaat	atgattgccc	gcctaaacaa	gtcagaactg	gcaacaggca	1440
gcagaccata	aaatatattt	agagaaagac	tattctgtct	attaagataa	attgataaag	1500
ctataaaata	aagaggctct	gcaggataaa	acagggtttac	gttcaccatc	gtaacagcaa	1560
tcattatcag	aaaattgctt	atcgaaaaaa	gagttaattc	ctttttcgat	aaagtgacat	1620
tacttacctt	agaaaataga	aacaagagaa	atagaacggt	tagataagtt	aataaaccat	1680
ttgaaagtat	cattaaggct	tcattcattt	tgctctcctt	tgatcagcaa	tcacagctct	1740
cagttttgtt	aacttagttc	gtgaaataag	acaagactta	ttatttcgaa	aataggccaa	1800
gcgttttttc	cgatcaatac	gggtaatat	ggcaggattg	acaataaaag	agcgatggca	1860
ctgaaaaagt	ctcttatcca	ttttaacaat	gtcagtcata	ctgccgtaga	attcaatccg	1920
ttcatcataa	gtataaaggc	agagcttatg	ggctgttgaa	gatgtttcaa	aatacagaat	1980
ctcagcaaaa	gggacctgaa	actgagtttc	agatgaatgg	aaaataaaaa	gttcctctga	2040
ttgaccattc	ttctggctgt	tttccatagc	ataatacagc	gctgattcaa	tgcggtggga	2100
gaactcctca	ggattcaaag	atztatcaat	aaaatccaaa	gcagatacct	gatactgaaa	2160
agtgaggggc	ataaactcag	aatgtgtcgt	gacaaagaca	ataactgcac	taggattatg	2220
ctgtctaate	tgattggcta	cttcagtc	tttcttttcc	tcttttttga	tttcaatctc	2280
caaaaagaaa	atctggtgat	tgcccttttc	agggatagcg	tcaataagtt	gttgtggttt	2340
tccaaaaata	gtcaattctt	tataagacca	atttttttct	ttcatgatag	ctgcaatggt	2400
ggtttcaaga	cgtccttggt	gtaaaaaatc	atcttccaat	acaaaaatag	aatcattat	2460
ttctccttta	atcttctatt	taggttagct	gattaacact	atacacagaa	aaggataaaa	2520
acgatatcac	tcaataaaat	ctactaactt	aataacc			2557

<210> 22

<211> 480

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(408)

<400> 22

atg gaa gaa gat ttt gaa att gtt ttt aat aag gtt aag cca att gta 48
Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val
1 5 10 15

tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438
Glu Leu Phe Glu Arg Leu Val Ala
130 135

ctgaaagatt tacgtaaaaa attaagtgat ttttaaggaaa aa 480

<210> 23

<211> 136

<212> PRT

<213> Streptococcus mutans

<400> 23

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val
1 5 10 15

Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala
130 135

<210> 24

<211> 680

<212> DNA

<213> Streptococcus mutans

<220>

<221> misc_feature

<222> (1)..(680)

<400> 24
gtaaataaaa cagccagtta agatgggaca tttatgtcct gttcttaaag tctttttcgt 60
tttataataa ttttattata aaaggagggtc atcgtaatag atggaagaag attttgaaat 120
tgtttttaaat aagggttaagc caattgtatg gaaattaagc cgttattact ttattaaaaat 180
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240
acatccagaa ttagaagagg atgatacaaa attgtatatc tattttaaga cacgtttttc 300
taattacatt aaagatgttt tgcgtcagca agaaagtcag aaacgtcggt ttaatagaat 360
gtcttatgaa gaagtcggtg agattgaaca ctgtttgtca agtggcggtg tgcaattgga 420
tgaatatatt ttatttcgtg atagtttgct tgcataataa caaggtctga gtactgaaaa 480
gcaagagctg tttgagcgtc tggtagcagg agagcacttt ttgggaaggc aaagtatgct 540
gaaagattta cgtaaaaaat taagtgattt taaggaaaaa tagttaaaaa gggaaagaat 600
ggaacatgtg attgtaccat tctttttggt tgaaaattaa gaaaagttat tataaattat 660
tggtttaaca tgccatatta 680

<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(2280)

<400> 25
atg aaa caa gtt att tat gtt gtt tta atc gtc ata gcc gtt aac att 48
Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15
ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30
tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg

35	40	45	
cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca			192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala			
50	55	60	
gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct			240
Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala			
65	70	75	80
tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt			288
Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu			
	85	90	95
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc			336
Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile			
	100	105	110
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt			384
Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe			
	115	120	125
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc			432
Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val			
	130	135	140
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca			480
Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser			
145	150	155	160
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca			528
Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr			
	165	170	175
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa			576
Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys			
	180	185	190
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag			624
Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln			
	195	200	205
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc			672
Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu			
	210	215	220
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac			720
Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr			
225	230	235	240
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg			768
Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu			
	245	250	255
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac			816
Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr			
	260	265	270

ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct	864
Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser	
275 280 285	
tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg	912
Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg	
290 295 300	
cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att	960
Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile	
305 310 315 320	
gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg	1008
Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met	
325 330 335	
gta att ttg gtt ggt ggg gtt ttg ttg gcg caa aac aat aac ctt ttc	1056
Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe	
340 345 350	
ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct	1104
Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala	
355 360 365	
ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat	1152
Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn	
370 375 380	
gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc	1200
Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr	
385 390 395 400	
att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt	1248
Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser	
405 410 415	
gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt	1296
Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser	
420 425 430	
gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt	1344
Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val	
435 440 445	
gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca	1392
Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser	
450 455 460	
gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat	1440
Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn	
465 470 475 480	
cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc	1488
Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg	
485 490 495	

gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt	1536
Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe	
500 505 510	
gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att	1584
Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile	
515 520 525	
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta	1632
Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu	
530 535 540	
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt	1680
Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val	
545 550 555 560	
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat	1728
Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn	
565 570 575	
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta	1776
Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu	
580 585 590	
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg	1824
Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro	
595 600 605	
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta	1872
Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu	
610 615 620	
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa	1920
Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu	
625 630 635 640	
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag	1968
Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln	
645 650 655	
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg	2016
Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg	
660 665 670	
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg	2064
Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu	
675 680 685	
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc	2112
Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile	
690 695 700	
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac	2160
Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His	
705 710 715 720	
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag	2208

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa 2256
Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

ggt ttc tat tat aac ctg ttt aat 2280
Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val

130		135		140
Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser				
145		150		155 160
Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr				
	165		170	175
Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys				
	180		185	190
Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln				
	195		200	205
Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu				
	210		215	220
Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr				
225		230		235 240
Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu				
	245		250	255
Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr				
	260		265	270
Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser				
	275		280	285
Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg				
290		295		300
Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile				
305		310		315 320
Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met				
	325		330	335
Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe				
	340		345	350
Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala				
	355		360	365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
 370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
 385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
 405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
 420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
 515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
 530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
 545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
 565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
 580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 27

<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(900)

<400> 27

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Met	Asp	Pro	Lys	Phe	Leu	Gln	Ser	Ala	Glu	Phe	Tyr	Arg	Arg	Arg	Tyr	
1			5					10				15				

cat	aat	ttt	gcg	aca	cta	tta	att	ggt	cct	ttg	gtc	tgc	ttg	att	atc	96
His	Asn	Phe	Ala	Thr	Leu	Leu	Ile	Val	Pro	Leu	Val	Cys	Leu	Ile	Ile	
			20					25				30				

ttc	ttg	gtc	ata	ttc	ctt	tgt	ttt	gct	aaa	aaa	gaa	att	aca	gtg	att	144
Phe	Leu	Val	Ile	Phe	Leu	Cys	Phe	Ala	Lys	Lys	Glu	Ile	Thr	Val	Ile	
		35					40				45					

tct	act	ggg	gaa	gtt	gca	cca	aca	aag	ggt	gta	gat	ggt	atc	caa	tct	192
Ser	Thr	Gly	Glu	Val	Ala	Pro	Thr	Lys	Val	Val	Asp	Val	Ile	Gln	Ser	
	50				55						60					

tac	agt	gac	agt	tca	atc	att	aaa	aat	aat	tta	gat	aat	aat	gca	gct	240
Tyr	Ser	Asp	Ser	Ser	Ile	Ile	Lys	Asn	Asn	Leu	Asp	Asn	Asn	Ala	Ala	
65					70					75				80		

gtt	gag	aag	gga	gac	gtt	tta	att	gaa	tat	tca	gaa	aat	gcc	agt	cca	288
Val	Glu	Lys	Gly	Asp	Val	Leu	Ile	Glu	Tyr	Ser	Glu	Asn	Ala	Ser	Pro	
			85					90				95				

aac	cgt	cag	act	gaa	caa	aag	aat	att	ata	aaa	gaa	aga	caa	aaa	cga	336
Asn	Arg	Gln	Thr	Glu	Gln	Lys	Asn	Ile	Ile	Lys	Glu	Arg	Gln	Lys	Arg	
		100					105					110				

gaa	gag	aag	gaa	aag	aaa	aaa	cac	caa	aag	agc	aag	aaa	aag	aag	aag	384
Glu	Glu	Lys	Glu	Lys	Lys	Lys	His	Gln	Lys	Ser	Lys	Lys	Lys	Lys	Lys	
		115					120				125					

tct	aag	agc	aag	aaa	gct	tcc	aaa	gat	aag	aaa	aag	aaa	tcg	aaa	gac	432
Ser	Lys	Ser	Lys	Lys	Ala	Ser	Lys	Asp	Lys	Lys	Lys	Lys	Ser	Lys	Asp	
	130				135						140					

aag	gaa	agc	agc	tct	gac	gat	gaa	aat	gag	aca	aaa	aag	gtt	tcg	att	480
Lys	Glu	Ser	Ser	Ser	Asp	Asp	Glu	Asn	Glu	Thr	Lys	Lys	Val	Ser	Ile	
145					150				155				160			

ttt	gct	tca	gaa	gat	ggg	att	att	cat	acc	aat	ccc	aaa	tat	gat	ggg	528
Phe	Ala	Ser	Glu	Asp	Gly	Ile	Ile	His	Thr	Asn	Pro	Lys	Tyr	Asp	Gly	
			165					170					175			

gcc	aat	att	att	ccg	aag	caa	acc	gag	att	gct	caa	atc	tat	cct	gat	576
Ala	Asn	Ile	Ile	Pro	Lys	Gln	Thr	Glu	Ile	Ala	Gln	Ile	Tyr	Pro	Asp	
		180						185				190				

att	caa	aaa	aca	aga	aaa	gtg	tta	atc	acc	tat	tat	gct	tct	tct	gat	624
Ile	Gln	Lys	Thr	Arg	Lys	Val	Leu	Ile	Thr	Tyr	Tyr	Ala	Ser	Ser	Asp	

195	200	205	
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa			672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu			
210	215	220	
aaa aag gga aat gac aag gtt gtt att gaa gga aaa att aac aat gtc			720
Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val			
225	230	235	240
gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act			768
Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr			
245	250	255	
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt			816
Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly			
260	265	270	
atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat			864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp			
275	280	285	
tat ttc aaa gat aaa tta ctg cat aaa atg gat aat			900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn			
290	295	300	

<210> 28

<211> 300

<212> PRT

<213> Streptococcus mutans

<400> 28

Met	Asp	Pro	Lys	Phe	Leu	Gln	Ser	Ala	Glu	Phe	Tyr	Arg	Arg	Arg	Tyr
1				5					10					15	

His	Asn	Phe	Ala	Thr	Leu	Leu	Ile	Val	Pro	Leu	Val	Cys	Leu	Ile	Ile
			20					25					30		

Phe	Leu	Val	Ile	Phe	Leu	Cys	Phe	Ala	Lys	Lys	Glu	Ile	Thr	Val	Ile
		35					40					45			

Ser	Thr	Gly	Glu	Val	Ala	Pro	Thr	Lys	Val	Val	Asp	Val	Ile	Gln	Ser
	50						55				60				

Tyr	Ser	Asp	Ser	Ser	Ile	Ile	Lys	Asn	Asn	Leu	Asp	Asn	Asn	Ala	Ala
65					70					75				80	

